

RAW SEQUENCE LISTING

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Application Serial Number: 10/507,132
Source: PCT
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RAW SEQUENCE LISTING

DATE: 04/11/2006

PATENT APPLICATION: US/10/507,132

TIME: 12:29:51

Input Set : A:\2005-06-06 1254-0258PUS1.ST25.txt

Output Set: N:\CRF4\04112006\J507132.raw

3 <110> APPLICANT: Koichiro KAKU et al.

5 <120> TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE

TO

6 AGRICULTURAL FUNGICIDAL AGENT

8 <130> FILE REFERENCE: 1254-0258PUS1

10 <140> CURRENT APPLICATION NUMBER: US 10/507,132

11 <141> CURRENT FILING DATE: 2004-09-10

13 <150> PRIOR APPLICATION NUMBER: JP 2002-66955

14 <151> PRIOR FILING DATE: 2002-03-12

16 <160> NUMBER OF SEQ ID NOS: 19

18 <170> SOFTWARE: PatentIn ver. 2.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 516

22 <212> TYPE: DNA

23 <213> ORGANISM: Pyricularia oryzae

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (1)..(516)

29 <400> SEQUENCE: 1

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32   1               5               10              15
34 ctg ggc ctc atg act tgc gtc tat gag tgg gca gac agc tac gac tcc      96
35 Leu Gly Leu Met Thr Cys Val Tyr Glu Trp Ala Asp Ser Tyr Asp Ser
36           20           25           30
38 aag gac tgg gat agg ctg cga aag gtc att gcg cct act ctg cgc att      144
39 Lys Asp Trp Asp Arg Leu Arg Lys Val Ile Ala Pro Thr Leu Arg Ile
40       35       40       45
42 gac tac cgc tcc ttc ctc gac aag ctc tgg gag gca atg ccg gcc gag      192
43 Asp Tyr Arg Ser Phe Leu Asp Lys Leu Trp Glu Ala Met Pro Ala Glu
44   50           55           60
46 gag ttc gtc ggc atg gtc tcg agc aag cag atg ctg ggc gac ccc acc      240
47 Glu Phe Val Gly Met Val Ser Ser Lys Gln Met Leu Gly Asp Pro Thr
48  65           70           75           80
50 ctc cgc acg cag cac ttc atc ggc ggc acg cgc tgg gag aag gtg tcc      288
51 Leu Arg Thr Gln His Phe Ile Gly Gly Thr Arg Trp Glu Lys Val Ser
52           85           90           95
54 gag gac gag gtc atc ggc tac cac cag ctg cgc gtc ccg cac cag agg      336
55 Glu Asp Glu Val Ile Gly Tyr His Gln Leu Arg Val Pro His Gln Arg
56       100       105       110
58 tac aag gac acc acc atg aag gag gtc acc atg aag ggc cac gcc cac      384
59 Tyr Lys Asp Thr Thr Met Lys Glu Val Thr Met Lys Gly His Ala His
60       115       120       125
62 tcg gca aac ctt cac tgg tac aag aag atc gac ggc gtc tgg aag ttc      432

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63 Ser Ala Asn Leu His Trp Tyr Lys Lys Ile Asp Gly Val Trp Lys Phe
64      130                      135                      140
66 gcc ggc ctc aag ccc gat atc cgc tgg ggc gag ttc gac ttt gac agg      480
67 Ala Gly Leu Lys Pro Asp Ile Arg Trp Gly Glu Phe Asp Phe Asp Arg
68 145                      150                      155                      160
70 atc ttt gag gac gga cgg gag acc ttt ggc gac aaa                      516
71 Ile Phe Glu Asp Gly Arg Glu Thr Phe Gly Asp Lys
72      165                      170
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76 <211> LENGTH: 172
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84 Leu Gly Leu Met Thr Cys Val Tyr Glu Trp Ala Asp Ser Tyr Asp Ser
85      20      25      30
87 Lys Asp Trp Asp Arg Leu Arg Lys Val Ile Ala Pro Thr Leu Arg Ile
88      35      40      45
90 Asp Tyr Arg Ser Phe Leu Asp Lys Leu Trp Glu Ala Met Pro Ala Glu
91      50      55      60
93 Glu Phe Val Gly Met Val Ser Ser Lys Gln Met Leu Gly Asp Pro Thr
94      65      70      75      80
96 Leu Arg Thr Gln His Phe Ile Gly Gly Thr Arg Trp Glu Lys Val Ser
97      85      90      95
99 Glu Asp Glu Val Ile Gly Tyr His Gln Leu Arg Val Pro His Gln Arg
100      100      105      110
102 Tyr Lys Asp Thr Thr Met Lys Glu Val Thr Met Lys Gly His Ala His
103      115      120      125
105 Ser Ala Asn Leu His Trp Tyr Lys Lys Ile Asp Gly Val Trp Lys Phe
106      130      135      140
108 Ala Gly Leu Lys Pro Asp Ile Arg Trp Gly Glu Phe Asp Phe Asp Arg
109 145      150      155      160
111 Ile Phe Glu Asp Gly Arg Glu Thr Phe Gly Asp Lys
112      165      170
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117 <211> LENGTH: 516
118 <212> TYPE: DNA
119 <213> ORGANISM: Pyricularia oryzae
121 <220> FEATURE:
122 <221> NAME/KEY: CDS
123 <222> LOCATION: (1)..(516)
125 <400> SEQUENCE: 3
126 atg ggt tgc caa gtt caa aag agc gat gag ata acc ttc tca gac tac      48
127 Met Gly Ser Gln Val Gln Lys Ser Asp Glu Ile Thr Phe Ser Asp Tyr
128      1      5      10      15
130 ctg ggc ctc atg act tgc gtc tat gag tgg gca gac agc tac gac tcc      96
131 Leu Gly Leu Met Thr Cys Val Tyr Glu Trp Ala Asp Ser Tyr Asp Ser
132      20      25      30

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134 aag gac tgg gat agg ctg cga aag gtc att gcg cct act ctg cgc att 144
135 Lys Asp Trp Asp Arg Leu Arg Lys Val Ile Ala Pro Thr Leu Arg Ile
136      35      40      45
138 gac tac cgc tcc ttc ctc gac aag ctc tgg gag gca atg ccg gcc gag 192
139 Asp Tyr Arg Ser Phe Leu Asp Lys Leu Trp Glu Ala Met Pro Ala Glu
140      50      55      60
142 gag ttc gtc ggc atg gtc tcg agc aag cag gtg ctg ggc gac ccc acc 240
143 Glu Phe Val Gly Met Val Ser Ser Lys Gln Val Leu Gly Asp Pro Thr
144      65      70      75      80
146 ctc cgc acg cag cac ttc atc ggc ggc acg cgc tgg gag aag gtg tcc 288
147 Leu Arg Thr Gln His Phe Ile Gly Gly Thr Arg Trp Glu Lys Val Ser
148      85      90      95
150 gag gac gag gtc atc ggc tac cac cag ctg cgc gtc ccg cac cag agg 336
151 Glu Asp Glu Val Ile Gly Tyr His Gln Leu Arg Val Pro His Gln Arg
152      100     105     110
154 tac aag gac acc acc atg aag gag gtc acc atg aag ggc cac gcc cac 384
155 Tyr Lys Asp Thr Thr Met Lys Glu Val Thr Met Lys Gly His Ala His
156      115     120     125
158 tgg gca aac ctt cac tgg tcc aag aag atc gac ggc gtc tgg aag ttc 432
159 Ser Ala Asn Leu His Trp Tyr Lys Lys Ile Asp Gly Val Trp Lys Phe
160      130     135     140
162 gcc ggc ctc aag ccc gat atc cgc tgg ggc gag ttc gac ttt gac agg 480
163 Ala Gly Leu Lys Pro Asp Ile Arg Trp Gly Glu Phe Asp Phe Asp Arg
164      145     150     155     160
166 atc ttt gag gac gga cgg gag acc ttt ggc gac aaa 516
167 Ile Phe Glu Asp Gly Arg Glu Thr Phe Gly Asp Lys
168      165     170
171 <210> SEQ ID NO: 4
172 <211> LENGTH: 172
173 <212> TYPE: PRT
174 <213> ORGANISM: Pyricularia oryzae
176 <400> SEQUENCE: 4
177 Met Gly Ser Gln Val Gln Lys Ser Asp Glu Ile Thr Phe Ser Asp Tyr
178      1      5      10      15
180 Leu Gly Leu Met Thr Cys Val Tyr Glu Trp Ala Asp Ser Tyr Asp Ser
181      20      25      30
183 Lys Asp Trp Asp Arg Leu Arg Lys Val Ile Ala Pro Thr Leu Arg Ile
184      35      40      45
186 Asp Tyr Arg Ser Phe Leu Asp Lys Leu Trp Glu Ala Met Pro Ala Glu
187      50      55      60
189 Glu Phe Val Gly Met Val Ser Ser Lys Gln Val Leu Gly Asp Pro Thr
190      65      70      75      80
192 Leu Arg Thr Gln His Phe Ile Gly Gly Thr Arg Trp Glu Lys Val Ser
193      85      90      95
195 Glu Asp Glu Val Ile Gly Tyr His Gln Leu Arg Val Pro His Gln Arg
196      100     105     110
198 Tyr Lys Asp Thr Thr Met Lys Glu Val Thr Met Lys Gly His Ala His
199      115     120     125
201 Ser Ala Asn Leu His Trp Tyr Lys Lys Ile Asp Gly Val Trp Lys Phe

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202      130      135      140
204 Ala Gly Leu Lys Pro Asp Ile Arg Trp Gly Glu Phe Asp Phe Asp Arg
205 145      150      155      160
207 Ile Phe Glu Asp Gly Arg Glu Thr Phe Gly Asp Lys
208      165      170
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 21
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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219 <400> SEQUENCE: 5
220 gcagtgtatc ccacacccaa g 21
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 22
225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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231 <400> SEQUENCE: 6
232 ttatttggtc gcaaaggtct cc 22
235 <210> SEQ ID NO: 7
236 <211> LENGTH: 44
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
primer
243 <400> SEQUENCE: 7
244 agttcgaact ggaattcaac cggcacgcat gatgcatgca tttt 44
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 21
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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255 <400> SEQUENCE: 8
256 atgggttcgc aagttcaaaa g 21
259 <210> SEQ ID NO: 9
260 <211> LENGTH: 23
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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267 <400> SEQUENCE: 9
268 gtggcccttc atggtgacct cct 23
271 <210> SEQ ID NO: 10
272 <211> LENGTH: 20
273 <212> TYPE: DNA

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274 <213> ORGANISM: Artificial Sequence

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276 <220> FEATURE:
277 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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291 <400> SEQUENCE: 11
292 atcgctcgacg tgaattcgtc ttgtaaaagc cgccaac 37
295 <210> SEQ ID NO: 12
296 <211> LENGTH: 27
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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303 <400> SEQUENCE: 12
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307 <210> SEQ ID NO: 13
308 <211> LENGTH: 600
309 <212> TYPE: DNA
310 <213> ORGANISM: Pyricularia oryzae
312 <400> SEQUENCE: 13
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315 aacttgtaaa agccgccaac atgggttcgc aagttcaaaa gagcgatgag ataaccttct 120
317 cagactacct gggcctcatg acttgcgctc atgagtgggc agacagctac gactccaagg 180
319 actgggatag gctgcgaaag gtcattgcgc ctactctgcg cattgactac cgctccttcc 240
321 tcgacaagct ctgggaggga atgcccggcg aggagtctgt cggcatggtc tcgagcaagc 300
323 aggtgctggg cgaccccacc ctccgcacgc agcacttcac cggcggcacg cgctgggaga 360
325 aggtgtccga ggacgagggtc atcggtacc accagctgcg cgtcccgcac cagaggtaca 420
327 aggacaccac catgaaggag gtcaccatga agggccacgc ccactcggca aaccttcact 480
329 ggtacaagaa gatcgacggc gtctggaagt tcgccggcct caagcccgat atccgctggg 540
331 gcgagttcga ctttgacagg atctttgagg acggacggga gacctttggc gacaaataaa 600
334 <210> SEQ ID NO: 14
335 <211> LENGTH: 545
336 <212> TYPE: DNA
337 <213> ORGANISM: Pyricularia oryzae
339 <400> SEQUENCE: 14
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344 cagctacgac tccaaggact gggataggct gcgaaagggtc attgcgccta ctctgcgcac 180
346 tgactaccgc tcttctctcg acaagctctg ggaggcaatg ccggccgagg agttcgtcgg 240
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350 cggcacgcgc tgggagaagg tgtccgagga cgaggtcatc ggctaccacc agctgcgcgt 360
352 cccgcaccag aggtacaagg acaccacat gaaggagggt accatgaagg gccacgcccc 420
354 ctccgcaaac cttcactggg acaagaagat cgacggcggtc tgggaagttc ccggcctcaa 480
356 gcccgcacat cgctggggcg agttcgactt tgacaggatc tttgaggacg gacggggagac 540

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